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Proposed Amendments  
~~(XXXXXX)~~

Client Matter: 52441-20002.00

Currently Pending Claims

to

and identify

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13. A method to design primers ~~wherein said primers target~~ a first nucleotide sequence wherein the expression of said first nucleotide sequence results in at least one phenotypic characteristic, the method comprising the steps of:

providing a second nucleotide sequence that is known to result in the phenotypic characteristic wherein the first nucleotide sequence and second nucleotide sequence are derived from different species;

comparing the second nucleotide sequence to nucleotide sequences cataloged in one or more databases that annotate nucleotide sequences with phenotypic characteristics;

extracting any cataloged nucleotide sequences that contain a portion of the second nucleotide sequence and which are annotated with said phenotypic characteristic;

aligning the second nucleotide sequence to each extracted nucleotide sequence;

prioritizing according to statistical analysis the extracted nucleotide sequences based on at least percent similarity with sequences having the highest percent similarity being highest in priority to ensure alignment to the second nucleotide sequence as determined by said statistical analysis; and

designing one or more primers based on matching portions of the aligned prioritized sequences, ~~said portions being of sufficient length to~~ <sup>which</sup> target said first nucleotide sequence.

and identify

14. The method of claim 13, further comprising the step prior to the step of extracting cataloged nucleotide sequences of filtering the second nucleotide sequence to eliminate portions which are regions commonly found in encoding nucleotide sequences.

16. The method of claim 13, further comprising the step of cloning said first nucleotide sequence using the one or more designed primers.

17. The method of claim 13, wherein the one or more databases are selected from cataloged sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

19. The method of claim 13, wherein the one or more primers are nested.

25. The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

26. The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing the nucleotide sequences.